

## SEQUENCE LISTING:

<110> Leong, Steven R.  
Punnonen, Juha



<120> CYTOKINE POLYPEPTIDES AND NUCLEIC ACIDS

<130> 02-108010US

<150> 60/169,035

<151> 1999-12-02

<160> 44

<170> FastSEQ for Windows Version 4.0

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<212> DNA

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<220>

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gcccctggag aaatgggtgt cctcgcctgt gacactcctg aagaagatgg catcacctgg 180
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aaagagccca	aaaacaagag	ctttctaaaa	tgtgaggcaa	agaattactc	cggacgtttc	420
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ccagccgctg	aggagagcct	gcccattgag	gtcgtgctgg	aagctgttca	caagctcaag	660
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<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 4

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acctcagacc	agagcagtga	ggtcctgggc	actggcaaaa	ccctgaccat	ccacgtcaaa	240
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aaaaagccca	aaaacaagat	ctttctgaaa	tgtgaggcaa	agaattactc	cggacgtttc	420
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<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic Sequence

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Val Glu Leu Asp Trp Tyr Pro Asn Ala Pro Gly Glu Thr Val Val Leu  
35 40 45  
Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln  
50 55 60  
Ser Ser Glu Val Leu Gly Thr Gly Lys Thr Leu Thr Ile His Val Lys  
65 70 75 80  
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys Arg Lys Gly Gly Glu Ala  
85 90 95  
Leu Ser Arg Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp  
100 105 110  
Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Ser Phe  
115 120 125  
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140  
Leu Thr Thr Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160  
Gly Ser Thr Asp Pro Arg Gly Val Thr Cys Gly Thr Ala Thr Leu Ser  
165 170 175  
Glu Asp Leu Gly Glu Tyr Lys Lys Tyr Arg Val Glu Cys Gln Glu Gly  
180 185 190  
Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Leu





<210> 11  
 <211> 327  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

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 20 25 30  
 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Thr Val Val Leu  
 35 40 45  
 Ala Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Ser Asp Gln  
 50 55 60  
 Ser Ser Glu Val Leu Gly Thr Gly Lys Thr Leu Thr Ile His Val Lys  
 65 70 75 80  
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys Arg Lys Gly Gly Ala Val  
 85 90 95  
 Leu Ser Gln Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110  
 Ser Thr Asp Ile Leu Lys Asp Gln Lys Lys Pro Lys Asn Lys Ile Phe  
 115 120 125  
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140  
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
 145 150 155 160  
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
 165 170 175  
 Ala Glu Arg Val Ser Met Asp His Arg Glu Tyr Asn Lys Tyr Thr Val  
 180 185 190  
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
 195 200 205  
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220  
 Thr Ser Arg Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
 225 230 235 240  
 Asn Leu Gln Leu Arg Pro Leu Lys Asn Ser Arg His Val Glu Ile Ser  
 245 250 255  
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270  
 Thr Phe Cys Val Gln Val Gln Gly Lys Asn Lys Arg Glu Lys Lys Leu  
 275 280 285  
 Phe Met Asp Gln Thr Ser Ala Lys Val Thr Cys His Lys Asp Ala Lys  
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 Ile Arg Val Gln Ala Arg Asp Arg Tyr His Ser Ser Trp Ser Glu  
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 Trp Ala Ser Val Pro Cys Ser  
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<223> Synthetic Sequence

<400> 12

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			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
		35					40					45			
Ala	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Ser	Asp	Gln
	50					55					60				
Ser	Ser	Glu	Val	Leu	Gly	Thr	Gly	Lys	Thr	Leu	Thr	Ile	His	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val
			85						90					95	
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Glu	Pro	Lys	Asn	Lys	Ser	Phe
		115					120						125		
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Thr	Ile	Ser	Thr	Asp	Leu	Thr	Phe	Ser	Val	Lys	Ser	Ser	Arg
145					150					155					160
Gly	Ser	Thr	Asp	Pro	His	Gly	Val	Thr	Cys	Gly	Thr	Ala	Thr	Leu	Ser
			165						170					175	
Glu	Asp	Leu	Gly	Glu	Tyr	Lys	Lys	Tyr	Arg	Val	Glu	Cys	Gln	Glu	Gly
		180						185					190		
Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Leu
	195						200					205			
Glu	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe
	210					215					220				
Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	Leu	Arg
225					230					235					240
Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Asn	Trp	Glu	Tyr	Pro	Asp
			245						250					255	
Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Val	Gln
			260					265					270		
Val	Gln	Gly	Arg	Asn	Lys	Arg	Glu	Lys	Lys	Leu	Phe	Met	Asp	Gln	Thr
	275						280					285			
Ser	Ala	Lys	Val	Thr	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	Ala
	290					295					300				
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Cys	Gly														

<210> 13

<211> 324

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 13

Met	Cys	His	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Phe	Leu
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			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu







Cys	Gln	Glu	Asp	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile
	195						200					205			
Glu	Val	Met	Val	Asp	Ala	Val	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
	210					215					220				
Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225					230					235					240
Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	Gln	Val	Glu	Val	Ser	Trp
			245					250						255	
Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr
			260					265					270		
Phe	Cys	Val	Gln	Val	Gln	Gly	Lys	Ser	Lys	Arg	Glu	Lys	Lys	Asp	Arg
	275						280					285			
Val	Phe	Thr	Asp	Lys	Thr	Ser	Ala	Thr	Val	Ile	Cys	Arg	Lys	Asn	Ala
	290					295					300				
Ser	Ile	Ser	Val	Arg	Ala	Gln	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser
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Glu	Trp	Ala	Ser	Val	Pro	Cys	Ser								
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 gactactccc aaaacctgtt gaaggccgcc agcaacacgc ttcagaaggc cagacaaatt 180  
 ctagaatttt acccttgacac ttctgaggag atcgatcatg aagatatcac caaagataaa 240  
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 tccagagaga tctctctgat aactaatggg agttgcctgg cttccagaaa gacctctttt 360  
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 cagaagccct ccctggaaga actggatttt tataagacta aaatcaagct ctgcatactt 600  
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<400> 17  
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 cacctcagtt tgggcaggag cctccccacc accacagcaa gcccaggaag gagctgcctc 120  
 gactactccc aaaacctgtt gaaggccgcc agcaacacgc ttcagagggc cagacaaatt 180  
 ctagaatttt acccttgacac ttctgaggag atcgatcatg aagatatcac caaagataaa 240  
 accagcacag tggaggcctg tttaccactg gaattagcca cgaatgagag ttgcctggct 300  
 tccagagaga tctctctgat aactaatggg agttgcctgg cttccagaaa gacctctttt 360  
 atgacaaccc tgtgccttag cagcatctat gaggacttga agatgtacca gatggaattc 420  
 aaggccatga acgcaaagct tttgatggat cctaagaggc agatcttttt agatcaaaac 480  
 atgctggcag ttattgatga gctgatgcag gccctgaatt tcaacagtga gactgtgcca 540  
 cagaagccct ccctggaaga actggatttt tataagacta aaatcaagct ctgcatactt 600

cttcatgcct tcagaattcg ggcagtgacc atcaatagaa tgatgagcta tctgaattct 660  
tcctag 666

<210> 18

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 18

atgtgcccgc	cgcgcgccct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
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tcccaaaacc	tgctgagggc	cgtcagcaac	atgctgcaga	aggccagaca	aactctagaa	180
ttttactcct	gcacttccga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctgcttacc	actggaatta	atcaagaatg	agagttgcct	aaattccaga	300
gagacttctt	tcataactaa	tgggagttgc	ctagcctcca	gaaagacctc	ttttatgaca	360
accctgtgcc	ttagcagtat	ctatgaggac	ttgaagatgt	accaggtgga	gttcaagacc	420
atgaatgcaa	agcttctgat	gaatcctaag	aggcagatct	ttctggatca	aaacatgctg	480
acagctattg	atgagctggt	acaggccctg	aatttcaaca	gtgagactgt	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	acttcttcat	600
gcttttcagaa	ttcgggcagt	gaccatcaat	agaatgatga	gctatctgaa	ttcttccctag	660

<210> 19

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 19

atgtgtccag	cgcgcagcct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccctgt	ggccacccca	ggcccaggaa	tgctcccatg	ccttcaccac	120
tcccaaaacc	tgctgagggc	tgtcagcaac	acgctccaga	aggccaaaca	aaccctagaa	180
ttttaccctt	gcacttccga	agagattgat	catgaagata	tcacacaaga	taaaaccagc	240
acagtggagg	cctgtttacc	actggaatta	gccacgaatg	agagttgcct	ggcttccaga	300
gggatctctc	tgataactaa	tgggagttgc	ctggcctcca	gaaagacctc	ttttatgacg	360
accctgtgcc	ttagcagtat	ctatgaggac	ttgaagatgt	accaggtgga	gttcaaggcc	420
atgaatgcaa	agctgttaat	ggatcctaaa	aggcagatct	ttctggatca	aaacatgctg	480
gcagctattg	ctgagctaat	gcaggccctg	aatgtcaaca	gtgagactgc	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	acttcttcat	600
gcttttcagaa	ttcgtgcagt	gaccatcaat	agaatgatga	gctatctgaa	ttcttccctag	660

<210> 20

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 20

atgtgtccag	cgcgcagcct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccctgt	ggccacccca	ggcccaggaa	tggtcccatg	ccttcaccac	120
tcccaaaacc	tgctgagggc	cgtcagcaac	atgctgcaga	aggccagaca	aactctagaa	180
ttttactcct	gcacttccga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctgcttacc	actggaatta	atcaagaatg	agagttgcct	aaattccaga	300

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gagacttctt tcataactaa tgggagttgc cttagcctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaaggcc 420
atgaatgcaa agctgttaat ggatcctaaa aggcagatct ttctggatca aaacatgctg 480
gcagctattg ctgagctaata gcaggccctg aatgtcaaca gtgagactgc gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgtgcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 21  
 <211> 660  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

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<400> 21
atgtgtccag cgcgagcct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccccgt ggccactcca gaccaggaa tgttcccatg ccttcaccac 120
tcccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggcagaca aactctagaa 180
ttttactcct gcacttccga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc actggaatta gccacgaatg agagttgcct ggcttcaga 300
gggatctctc tgataactaa tgggagttgc cttagcctcca gaaagacctc ttttatgacg 360
accctgtgcc ttggcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 22  
 <211> 660  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

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<400> 22
atgtgcccgc cgcgcgccct cctccttgtg gctaccctgg tcctcctgga ccacctcagt 60
ttggccagaa acctccctgt ggccaccca ggcccaggaa tgttcccatg ccttcaccac 120
tcccaaaacc tgctgagggc cgtcagcaac atgctgcaga aggcagaca aactctagaa 180
ttttactcct gcacttccga agagactgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgcttacc actggaatta atcaagaatg agagttgcct aaattccaga 300
gagacttctt tcataactaa tgggagttgc cttagcctcca gaaagacctc ttttatgaca 360
accctgtgcc ttagcagtat ctatgaggac ttgaagatgt accaggtgga gttcaagacc 420
atgaatgcaa agcttctgat gaatcctaag aggcagatct ttctggatca aaacatgctg 480
acagctattg atgagctgtt acaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
gctttcagaa ttcgggcagt gaccatcaat agaatgatga gctatctgaa ttcttcctag 660

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<210> 23  
 <211> 660  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 23

atgtgcccgc	cgcgcgccct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccccgt	ggccacccca	ggcccaggaa	tggtcccatg	ccttcaccac	120
tcccaaaacc	tgctgagggc	tgtcagcaac	acgctccaga	aggccaaaca	aaccctagaa	180
ttttaccctt	gcacttccga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctggtttacc	actggaatta	gccacgaatg	agagttgcct	ggcttccaga	300
gggatctctc	tgataactaa	tgggagttgc	ctggcctcca	gaaagacctc	ttttatgaca	360
accctgtgcc	ttagcagcat	ctatgaggac	ttgaagatgt	accaggtgga	gttcaaggcc	420
atgaatgcaa	agctgttaat	ggatcctaaa	aggcagatct	ttctggatca	aaacatgctg	480
gcagctattg	ctgagctaat	gcaggccctg	aatgtcaaca	gtgagactgc	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	actttcttcat	600
gctttcagaa	ttcgggcagt	gaccatcaat	agaatgatga	gctatctgaa	ttcttcctag	660

<210> 24

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 24

atgtgtccag	cgcgcagcct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccccgt	ggccactcca	gacccaggaa	tggtcccatg	ccttcaccac	120
tcccaaaacc	tgctgagggc	tgtcagcaac	acgctccaga	aggccaaaca	aaccctagaa	180
ttttaccctt	gcacttccga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctggtttacc	actggaatta	gccacgaatg	agagttgcct	ggcttccaga	300
gggatctctc	tgataactaa	tgggagttgc	ctggcctcca	gaaagacctc	ttttatgacg	360
accctgtgcc	ttagcagcat	ctatgaggac	ttgaagatgt	accaggtgga	gttcaaggcc	420
atgaatgcaa	agctgttgat	ggatcctaaa	aggcagatct	ttctggatca	aaacatgctg	480
gcagctattg	ctgagctaat	gcaggccctg	aatgtcaaca	gtgagactgc	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataag	actaaaatca	agctctgcat	actttcttcat	600
gccttcagaa	ttcgtgcagt	gaccatcgat	agaatgatga	gctatctgaa	ttcttcctag	660

<210> 25

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 25

atgtgcccgc	cgcgcgccct	cctccttggt	gctaccctgg	tcctcctgga	ccacctcagt	60
ttggccagaa	acctccctgt	ggccacccca	ggcccaggaa	tggtcccatg	ccttcaccac	120
tcccaaaacc	tgctgagggc	cgtcagcaac	atgctgcaga	aggccagaca	aactctagaa	180
ttttactcct	gcacttccga	agagattgat	catgaagata	tcacaaaaga	taaaaccagc	240
acagtggagg	cctgcttacc	actggaatta	atcaagaatg	agagttgcct	aaattccaga	300
gagacttctt	tcataactaa	tgggagttgc	ctagcctcca	gaaagacctc	ttttatgaca	360
accctgtgcc	ttagcagtat	ctatgaggac	ttgaagatgt	accaggtgga	gttcaagacc	420
atgaatgcaa	agcttctgat	gaatcctaag	aggcagatct	ttctggatca	aaacatgctg	480
acagctattg	atgagctggt	acaggccctg	aatttcaaca	gtgagactgt	gccacaaaaa	540
tcctcccttg	aagaaccgga	tttttataaa	actaaaatca	agctctgcat	actttcttcat	600
gctttcagaa	ttcgggcagt	gaccatcaat	agaatgatga	gctatctgaa	ttcttcctag	660

<210> 26

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 26

Met	Cys	Pro	Leu	Arg	Ser	Leu	Leu	Leu	Ile	Ser	Thr	Leu	Val	Leu	Leu
1				5					10					15	
His	His	Leu	Pro	His	Leu	Ser	Leu	Gly	Arg	Ser	Leu	Pro	Thr	Thr	Thr
			20					25					30		
Ala	Ser	Pro	Gly	Arg	Ser	Cys	Leu	Asp	Tyr	Ser	Gln	Asn	Leu	Leu	Lys
		35					40					45			
Ala	Ala	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Ile	Leu	Glu	Phe	Tyr
	50					55					60				
Pro	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys
65					70					75					80
Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu
				85					90					95	
Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys
			100					105					110		
Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	His	Ser	Ser
		115					120					125			
Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met	Asn
	130					135					140				
Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn
145					150					155					160
Met	Leu	Ala	Val	Ile	Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser
				165					170					175	
Glu	Thr	Val	Pro	Gln	Lys	Pro	Ser	Leu	Glu	Glu	Leu	Asp	Phe	Tyr	Lys
			180					185					190		
Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala
		195					200					205			
Val	Thr	Ile	Asp	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser			
	210					215					220				

<210> 27

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 27

Met	Tyr	Pro	Leu	Arg	Ser	Leu	Leu	Leu	Ile	Ser	Thr	Leu	Val	Leu	Leu
1				5					10					15	
His	His	Leu	Pro	His	Leu	Ser	Leu	Gly	Arg	Ser	Leu	Pro	Thr	Thr	Thr
			20					25					30		
Ala	Ser	Pro	Gly	Arg	Ser	Cys	Leu	Asp	Tyr	Ser	Gln	Asn	Leu	Leu	Lys
		35					40					45			
Ala	Ala	Ser	Asn	Thr	Leu	Gln	Arg	Ala	Arg	Gln	Ile	Leu	Glu	Phe	Tyr
	50					55					60				
Pro	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys
65					70					75					80
Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu
				85					90					95	
Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys
			100					105					110		
Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser
		115					120					125			
Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Met	Glu	Phe	Lys	Ala	Met	Asn

130		135		140
Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn				
145		150		155
Met Leu Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser				160
	165		170	
Glu Thr Val Pro Gln Lys Pro Ser Leu Glu Glu Leu Asp Phe Tyr Lys				175
	180		185	
Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala				190
	195		200	
Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser				205
210		215		220

<210> 28  
 <211> 219  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 28

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Ala Thr Leu Val Leu Leu				
1	5	10	15	
Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Gly Pro				
	20	25	30	
Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val				
	35	40	45	
Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys				
	50	55	60	
Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser				
65	70	75	80	
Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ile Lys Asn Glu Ser Cys				
	85	90	95	
Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala				
	100	105	110	
Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr				
	115	120	125	
Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys				
	130	135	140	
Leu Leu Met Asn Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu				
145	150	155	160	
Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Glu Thr				
	165	170	175	
Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys				
	180	185	190	
Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr				
	195	200	205	
Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser				
210	215			

<210> 29  
 <211> 219  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 29



Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
		20						25					30		
Gly	Met	Leu	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
	35					40					45				
Ser	Asn	Thr	Leu	Gln	Lys	Ala	Lys	Gln	Thr	Leu	Glu	Phe	Tyr	Pro	Cys
	50					55					60				
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Gln	Asp	Lys	Thr	Ser
65				70						75				80	
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu	Ser	Cys
			85						90					95	
Leu	Ala	Ser	Arg	Gly	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
		100						105					110		
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr
	115						120					125			
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys
	130					135					140				
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145					150					155				160	
Ala	Ala	Ile	Ala	Glu	Leu	Met	Gln	Ala	Leu	Asn	Val	Asn	Ser	Glu	Thr
			165						170					175	
Ala	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
		180						185					190		
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
	195						200					205			
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser					
	210					215									

<210> 30

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic Sequence

<400> 30

Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
		20						25					30		
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
	35					40					45				
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys
	50					55					60				
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser
65				70						75				80	
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ile	Lys	Asn	Glu	Ser	Cys
			85						90					95	
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
		100						105					110		
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr
	115					120						125			
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys
	130					135					140				
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145					150					155				160	
Ala	Ala	Ile	Ala	Glu	Leu	Met	Gln	Ala	Leu	Asn	Val	Asn	Ser	Glu	Thr
			165						170					175	

Ala	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
			180					185					190		
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
		195					200					205			
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser					
	210						215								

<210> 31  
 <211> 219  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthetic Sequence

<400> 31															
Met	Cys	Pro	Ala	Arg	Ser	Leu	Leu	Leu	Val	Ala	Thr	Leu	Val	Leu	Leu
1				5					10					15	
Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Asp	Pro
		20					25						30		
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val
	35					40					45				
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys
	50				55					60					
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser
65				70					75					80	
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Ala	Thr	Asn	Glu	Ser	Cys
			85					90					95		
Leu	Ala	Ser	Arg	Gly	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala
		100					105					110			
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Gly	Ser	Ile	Tyr
	115					120					125				
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys
	130				135						140				
Leu	Leu	Met	Asn	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu
145				150					155					160	
Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr
			165					170						175	
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys
		180					185					190			
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr
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Asp	His	Leu	Ser	Leu	Ala	Arg	Asn	Leu	Pro	Val	Ala	Thr	Pro	Gly	Pro
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 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro  
 20 25 30  
 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val  
 35 40 45  
 Ser Asn Thr Leu Gln Lys Ala Lys Gln Thr Leu Glu Phe Tyr Pro Cys  
 50 55 60  
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
 65 70 75 80  
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ala Thr Asn Glu Ser Cys  
 85 90 95  
 Leu Ala Ser Arg Gly Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
 100 105 110  
 Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr  
 115 120 125  
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
 130 135 140  
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
 145 150 155 160  
 Ala Ala Ile Ala Glu Leu Met Gln Ala Leu Asn Val Asn Ser Glu Thr  
 165 170 175  
 Ala Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys  
 180 185 190  
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
 195 200 205  
 Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser  
 210 215

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 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val  
 35 40 45  
 Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys  
 50 55 60  
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
 65 70 75 80  
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Ile Lys Asn Glu Ser Cys

				85					90					95			
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala		
			100					105					110				
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr		
		115					120					125					
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys		
	130					135					140						
Leu	Leu	Met	Asn	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu		
145					150					155					160		
Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr		
			165						170					175			
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys		
		180						185					190				
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr		
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Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ser	Ser							
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		20					25					30					
Gly	Met	Phe	Pro	Cys	Leu	His	His	Ser	Gln	Asn	Leu	Leu	Arg	Ala	Val		
	35					40					45						
Ser	Asn	Met	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Pro	Cys		
	50				55					60							
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser		
65				70					75					80			
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Lys	Asn	Glu	Ser	Cys		
			85					90					95				
Leu	Asn	Ser	Arg	Glu	Thr	Ser	Phe	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala		
		100					105						110				
Ser	Arg	Lys	Thr	Ser	Phe	Met	Met	Ala	Leu	Cys	Leu	Ser	Ser	Ile	Tyr		
	115					120					125						
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Thr	Met	Asn	Ala	Lys		
	130					135					140						
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu		
145				150						155					160		
Ala	Val	Ile	Asp	Glu	Leu	Met	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Glu	Thr		
			165						170					175			
Val	Pro	Gln	Lys	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys		
		180						185					190				
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr		
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gcccctggag aaatggtggt cctcacctgt gacaccctg aagaagatgg tatcacctgg 180
accttggacc agagcagtga ggtcttaggc tctggcaaaa ccttgacat ccaagtcaaa 240
gagtttggag atgctggcca gtacacctgt cacaaggag gcgaggttct aagccattcg 300
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aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc 420
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gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat 660
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tcccaaaacc tgctgagggc cgtcagcaac atgctccaga aggccagaca aactctagaa 180
ttttaccctt gcacttctga agagattgat catgaagata tcacaaaaga taaaaccagc 240
acagtggagg cctgtttacc attggaatta accaagaatg agagttgcct aaattccaga 300
gagacctctt tcataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgatg 360
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atgaatgcaa agcttctgat ggatcctaag aggcatctt ttctagatca aaacatgctg 480
gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa 540
tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat 600
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			20					25					30		
Val	Glu	Leu	Asp	Trp	Tyr	Pro	Xaa	Ala	Pro	Gly	Glu	Xaa	Val	Val	Leu
		35					40					45			
Xaa	Cys	Asp	Thr	Pro	Glu	Glu	Asp	Gly	Ile	Thr	Trp	Thr	Xaa	Asp	Gln
	50					55					60				
Ser	Ser	Xaa	Val	Leu	Gly	Xaa	Gly	Lys	Thr	Leu	Thr	Ile	Xaa	Val	Lys
65					70					75					80
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	Xaa	Lys	Gly	Gly	Xaa	Xaa
			85						90					95	
Leu	Ser	Xaa	Ser	Leu	Leu	Leu	Leu	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Lys	Asp	Gln	Lys	Xaa	Pro	Lys	Xaa	Lys	Xaa	Phe
		115					120					125			
Leu	Xaa	Cys	Glu	Ala	Lys	Xaa	Tyr	Ser	Gly	Xaa	Phe	Thr	Cys	Trp	Trp
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Leu	Thr	Xaa	Ile	Ser	Thr	Asp	Leu	Xaa	Phe	Xaa	Val	Lys	Ser	Ser	Arg
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Gly	Ser	Xaa	Asp	Pro	Xaa	Gly	Val	Thr	Cys	Gly	Xaa	Xaa	Xaa	Leu	Ser
			165						170					175	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Val	Glu
			180					185					190		
Cys	Gln	Glu	Xaa	Ser	Ala	Cys	Pro	Xaa	Ala	Glu	Glu	Ser	Leu	Pro	Ile
		195					200					205			
Glu	Val	Xaa	Xaa	Xaa	Ala	Xaa	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr
	210				215						220				
Ser	Xaa	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn
225					230					235					240
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		260						265					270		
Phe	Xaa	Xaa	Gln	Val	Gln	Gly	Xaa	Xaa	Lys	Arg	Glu	Xaa	Xaa	Xaa	Xaa
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Xaa	Ile	Xaa	Val	Xaa	Ala	Xaa	Asp	Arg	Tyr	Xaa	Ser	Ser	Xaa	Trp	Ser
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 Xaa His Leu Ser Leu Xaa Arg Xaa Leu Pro Xaa Xaa Thr Xaa Xaa Pro  
 20 25 30  
 Gly Xaa Xaa Xaa Cys Leu Xaa Xaa Ser Gln Asn Leu Leu Xaa Ala Xaa  
 35 40 45  
 Ser Asn Xaa Leu Gln Xaa Ala Xaa Gln Xaa Leu Glu Phe Tyr Xaa Cys  
 50 55 60  
 Thr Ser Glu Glu Xaa Asp His Glu Asp Ile Thr Xaa Asp Lys Thr Ser  
 65 70 75 80  
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Xaa Xaa Asn Glu Ser Cys  
 85 90 95  
 Leu Xaa Ser Arg Xaa Xaa Ser Xaa Ile Thr Asn Gly Ser Cys Leu Ala  
 100 105 110  
 Ser Arg Lys Thr Ser Phe Met Xaa Xaa Leu Cys Xaa Xaa Ser Ile Tyr  
 115 120 125  
 Glu Asp Leu Lys Met Tyr Gln Xaa Glu Phe Lys Xaa Met Asn Ala Lys  
 130 135 140  
 Leu Leu Met Xaa Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
 145 150 155 160  
 Xaa Xaa Ile Xaa Glu Leu Xaa Gln Ala Leu Asn Xaa Asn Ser Glu Thr  
 165 170 175  
 Xaa Pro Gln Lys Xaa Ser Leu Glu Glu Xaa Asp Phe Tyr Lys Thr Lys  
 180 185 190  
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Val Trp Glu Ile Lys Lys Asp Met Tyr Val Val Glu Leu Glu Trp Tyr  
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Ala Ala Ala Gly Ala Pro Val Pro Tyr Pro Asp Pro Leu Glu Arg Ala  
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Ala Ala His His His His His  
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